

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 7, 2002, 16:03:52 ; Search time 180.87 Seconds

(without alignments)  
44.479 Million cell updates/sec

Title: US-08-569-749-5

Sequence: 1 CEIYKMSYTFPPAGVPSE.....KVKFCGGLMDNKKLGDSF 55

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP mhc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	301	98.0	1140	4 09UNH1	09unh1 homo sapien
2	298	97.1	602	11 09ESE9	09ese9 rattus norv
3	291	94.8	589	11 09QZC6	09qzc6 rattus norv
4	291	94.8	589	11 09ESE8	09ese8 rattus norv
5	247	80.5	324	13 09DDN2	09ddn2 gallus gall
6	247	80.5	410	13 057319	057319 gallus gall
7	152	49.5	496	11 09ESF0	09esf0 rattus norv
8	152	49.5	501	11 09E005	09e005 rattus norv
9	152	49.5	501	11 09E004	09e004 rattus norv
10	145	47.2	264	12 09E027	09e027 anascta moe
11	143	46.6	195	13 091A70	091a70 gallus gall
12	143	46.6	197	13 091A69	091a69 gallus gall
13	140	45.6	281	12 09YVL8	09ynl8 choristoneu
14	134	43.6	597	11 09R015	09r015 mus musculi
15	131	42.7	224	11 088642	088642 rattus norv
16	127	41.4	438	5 09VUX5	09vux5 drosophila
17	119	38.8	208	12 055770	055770 chilio fride
18	117	38.1	280	4 09HAP7	09hap7 homo sapien
19	117	38.1	298	4 09H2A8	09h2a8 homo sapien

20	113.5	37.0	153	5 09VEM2	09vem2 drosophila
21	111	36.2	313	12 09J827	09j827 spodoptera
22	107	34.9	379	5 09U492	09u492 trichoplus1
23	106	34.5	377	5 09M07	09m07 spodoptera
24	105.5	34.4	276	12 089744	089744 buzura supp
25	103	33.6	150	12 09YV4	09yv4 melanoplus
26	103	33.6	261	12 09EES9	09ees9 epiphyas po
27	101	32.9	268	12 09E232	09e232 helicoverpa
28	100	32.6	268	12 09F18	09f18 helicoverpa
29	92	30.0	301	12 09P254	09p254 trichoplus1
30	90	29.3	281	12 09DVT5	09dvt5 pluteia xy
31	88	28.7	87	11 009119	009119 mus musculi
32	87	28.3	285	12 09PY09	09py09 xestia c-ni
33	86.5	28.2	292	12 09P394	09p394 bombyx mori
34	84	27.4	87	11 009120	009120 mus musculi
35	84	27.4	87	11 009120	009120 mus musculi
36	83.5	27.2	187	12 09DSW8	09dsw8 ascovirus d
37	82	26.7	155	12 09YMT9	09ymt9 lymantria d
38	77.5	25.2	284	12 09YK15	09yk15 epiphyas po
39	73.5	23.9	137	4 09AVZ4	09avz4 homo sapien
40	72.5	23.6	142	6 09GLN5	09gln5 mus scrofa
41	71.5	23.3	484	11 098738	088738 mus musculi
42	69.5	22.0	4804	5 09YH01	09yh01 drosophila
43	68	22.5	250	12 093G75	093g75 helicoverp
44	68	22.1	428	12 093G77	093g77 helicoverp
45	65.5	21.3	234	12 09YMP8	09ymp8 lymantria d

#### ALIGNMENTS

RESULT 1  
ID 09UNH1 PRELIMINARY: PRT: 1140 AA.  
AC 09UNH1;  
DT 01-MAY-2000 (TRFMBIrel. 13, Created)  
DT 01-MAY-2000 (TRFMBIrel. 13, Last sequence update)  
DT 01-JUN-2001 (TRFMBIrel. 17, Last annotation update)  
DE AP12-MLT FUSION PROTEIN.  
GN AP12-MLT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9272400; PubMed=10339464;  
FA Dierramm J., Baens M., Wlodarska I., Stefanova-Ouzounova M.,  
FA Hernandez J.M., Hossfeld D.K., De Wolf-Peeters C., Hagemeijer A.,  
FA Van den Berghe H., Marynen P.;  
RT "The apoptosis inhibitor gene AP12 and a novel 18q gene, MLT, are  
RT recurrently rearranged in the t(11;18)(q21;q21)p66associated with  
RT mucosa-associated lymphoid tissue lymphomas.";  
RL Blood 93:3601-3609(1999).  
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN.  
CC EMBL: AF123094; AAD46161.1; .  
CC HSSP: Q13490; IOBH.  
DR InterPro: IPR001370; BIR.  
DR InterPro: IPR003576; Caspase.  
DR InterPro: IPR001309; ICE\_p20.  
DR InterPro: IPR003598; IG\_c2.  
DR InterPro: IPR003600; IG\_c2.  
DR InterPro: IPR003006; IG\_MHC.  
DR Pfam: PF00653; BIR; 3.  
DR Pfam: PF00047; IG; 2.  
DR SMART: SM00238; BIR; 3.  
DR SMART: SM00115; CASC; 1.  
DR SMART: SM00408; IGC2; 1.  
DR SMART: SM00410; IG\_Like; 1.  
DR PROSITE: PS01282; BIR\_REPEAT\_1; 3.  
DR PROSITE: PS0143; BIR\_REPEAT\_2; 3.  
DR PROSITE: PS0208; CASPASE\_P20; 1.





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DB      26 EBNRLKTFANFPSSSPVSASTLANRGLYTGCDTVOCFSCHAADVMOYGDS 78
      ZINC-finger.
RESULT  8
ID      09EQ05      PRELIMINARY:      PRT:      501 AA.
AC      09EQ05;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      INHIBITOR OF APOPTOSIS PROTEIN 3.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MISTAR; TISSUE=OVARY;
RA      Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT      Cloning, characterization and regulation of an inhibitor of apoptosis
RT      protein in the rat corpus luteum.
RT      Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
EMBL; AF304333; AAC41192.1; -.
CC      InterPro: IPR001841; znf_ring.
DR      Pfam: PF00653; zfc3hc4; 1.
DR      SMART: SM00238; BIR; 3.
DR      PROSITE: PS01282; BIR_REPEAT_1; 1.
DR      PROSITE: PS01443; BIR_REPEAT_2; 3.
KW      ZINC-finger.
SQ      SEQUENCE 501 AA: 56548 MW: 0973BF28E81C5A0 CRC64;
      Query Match      49.5%; Score 152; DB 11; Length 501;
      Best Local Similarity 50.9%; Pred. No. 2,8e-11;
      Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

OY      2 ELYRSTYSTFPAGVPYSEBSILANRAGFYTYGVNDKVCFCGGLMDNMKLGDS 54
      1 1 : : : : 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      26 EBNRLKTFANFPSSSPVSASTLANRGLYTGCDTVOCFSCHAADVMOYGDS 78

RESULT  9
ID      09EQ04      PRELIMINARY:      PRT:      501 AA.
AC      09EQ04;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      INHIBITOR OF APOPTOSIS PROTEIN 3.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MISTAR; TISSUE=OVARY;
RA      Lareu R.R., Bradley C.K., Lacher M., Ellis R.R., Dharmarajan A.M.;
RT      Cloning, characterization and regulation of an inhibitor of apoptosis
RT      protein in the rat corpus luteum.
RT      Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
EMBL; AF304333; AAC41193.1; -.
CC      InterPro: IPR001370; BIR.
DR      Pfam: PF00653; BIR; 3.
DR      SMART: SM00238; BIR; 3.
DR      PROSITE: PS01282; BIR_REPEAT_1; 1.

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DR      PROSITE: PS01443; BIR_REPEAT_2; 3.
KW      ZINC-finger.
SQ      SEQUENCE 501 AA: 56578 MW: 4863F69F2E0C8CD CRC64;

      Query Match      49.5%; Score 152; DB 11; Length 501;
      Best Local Similarity 50.9%; Pred. No. 2,8e-11;
      Matches 27; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

OY      2 ELYRSTYSTFPAGVPYSEBSILANRAGFYTYGVNDKVCFCGGLMDNMKLGDS 54
      1 1 : : : : 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      DB      26 EBNRLKTFANFPSSSPVSASTLANRGLYTGCDTVOCFSCHAADVMOYGDS 78

RESULT  10
ID      09EN27      PRELIMINARY:      PRT:      264 AA.
AC      09EN27;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      AMV021.
GN      AMV021.
OS      Musca domestica (Housefly).
OC      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC      Entomopoxvirus B.
OX      NCBI_TaxID=28321;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      REDLIND-20396580; PubMed=10936094;
RA      Bowden A.L., Glassberg R.J., Diggins J., Shaw R., Farmerie W.,
RA      Kozlovskiy M., Glassberg R.J., Diggins J., Shaw R., Farmerie W.,
RT      "Complete Sequence of the Musca domestica Entomopoxvirus:
RT      Analysis and Comparison with Other Poxviruses."
RT      Virology 274:120-139(2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Bowden A.L., Glassberg R.J., Diggins J., Shaw R., Farmerie W.,
RA      Moyer R.W.;
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF250284; AAC62727.1; -.
DR      InterPro: IPR001370; BIR.
DR      InterPro: IPR001841; znf_ring.
DR      Pfam: PF00653; BIR; 2.
DR      SMART: SM00238; BIR; 2.
DR      SMART: SM00184; RING; 1.
DR      PROSITE: PS01443; BIR_REPEAT_2; 2.
SQ      SEQUENCE 264 AA: 30547 MW: 2EB72DA4B58D920A CRC64;

      Query Match      47.2%; Score 145; DB 12; Length 264;
      Best Local Similarity 49.0%; Pred. No. 1.1e-10;
      Matches 25; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

OY      5 RMSYSTYSTFPAGVPYSEBSILANRAGFYTYGVNDKVCFCGGLMDNMKLGDS 55
      1 1 : : : : 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      DB      110 RUKYKEMPISTPSTKELNAGFFYOKSKVCFCGGLNKKWETDDP 160

RESULT  11
ID      09IA70      PRELIMINARY:      PRT:      195 AA.
AC      09IA70;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      INHIBITOR OF APOPTOSIS 1 (FRAGMENT).
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]

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RP SEQUENCE FROM N.A.  
 RC STRAIN-BREED LECHORN: TISSUE-SPLEEN;  
 RA Zhou H., Lamont S.J.;  
 RT \*Genetic variation among chicken lines and mammalian species in  
 RT specific genes.\*;  
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF221082; AAF35319.1; -  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR: 2.  
 DR SMART: SM00238; BIR: 2.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PSS0143; BIR\_REPEAT\_2; 2.  
 FT NON\_TER 1  
 FT 195  
 SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 46.6%; Score 143; DB 13; Length 195;  
 Best Local Similarity 51.0%; Pred. No. 1.5e-10;  
 Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 5 RMSYSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNMKLGDSF 55  
 DB 119 RVKFTINMPTRIPIQPEQLADAGFYTYGVNDKVCFCGGLMCRHESGDDP 169

RESULT 12  
 O91A69 PRELIMINARY: PRT; 197 AA.  
 AC 091A69;  
 DT 01-OCT-2000 (TReMBLrel. 15; Created)  
 DT 01-OCT-2000 (TReMBLrel. 15; Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17; Last annotation update)  
 DE INHIBITOR OF APOPTOSIS 1 (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus  
 OX NCBI\_TaxID=9031;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BREED FAYOUI: TISSUE-SPLEEN;  
 RA Zhou H., Lamont S.J.;  
 RT \*Genetic variation among chicken lines and mammalian species in  
 RT specific genes.\*;  
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF221083; AAF35320.1; -  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR: 2.  
 DR SMART: SM00238; BIR: 2.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PSS0143; BIR\_REPEAT\_2; 2.  
 FT NON\_TER 1  
 FT 197  
 SQ SEQUENCE 197 AA; 22602 MW; D7923DABC623E1A CRC64;

Query Match 46.6%; Score 143; DB 13; Length 197;  
 Best Local Similarity 51.0%; Pred. No. 1.5e-10;  
 Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 5 RMSYSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNMKLGDSF 55  
 DB 120 RVKFTINMPTRIPIQPEQLADAGFYTYGVNDKVCFCGGLMCRHESGDDP 170

RESULT 13  
 O9YVL8 PRELIMINARY: PRT; 281 AA.  
 AC 09YVL8;  
 DT 01-MAY-1999 (TReMBLrel. 10; Created)  
 DT 01-MAY-1999 (TReMBLrel. 10; Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17; Last annotation update)

DE IAP PROTEIN.  
 GN IAP.  
 OS Choriostoma fumihera nuclear polyhedrosis virus (CFMNPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=10448;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Ireland;  
 RA Lauzon H., Arif B.M., Ladd T., Palli R.;  
 RT \*cfmnpv iap gene.\*;  
 RT Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.  
 DR EMBL: U82510; AAD00537.1; -  
 DR HSSP: O13490; 10BH.  
 DR InterPro: IPR001370; BIR.  
 DR InterPro: IPR001841; ZnF\_Fing.  
 DR Pfam: PF00653; BIR: 2; ZincFinger.  
 DR SMART: SM00238; BIR: 2.  
 DR SMART: SM00184; RING\_1.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_1.  
 DR PROSITE: PSS0143; BIR\_REPEAT\_2; 2.  
 KM ZINC-FINGER.  
 SQ SEQUENCE 281 AA; 32090 MW; B2D9B8BA359F105E CRC64;

Query Match 45.6%; Score 140; DB 12; Length 281;  
 Best Local Similarity 46.1%; Pred. No. 5.3e-10;  
 Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 2 ELYRSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNMKLGDSF 55  
 DB 124 EBARLRTETPMRGLKQRPKEALVAGFYTYGVNDKVCFCGGLMDNMGDDP 177

RESULT 14  
 O9R015 PRELIMINARY: PRT; 597 AA.  
 AC 09R015;  
 DT 01-MAY-2000 (TReMBLrel. 13; Created)  
 DT 01-MAY-2000 (TReMBLrel. 13; Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17; Last annotation update)  
 DE NEURONAL APOPTOSIS INHIBITORY PROTEIN.  
 GN BIRCLE OR NAIIP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=9431676; PubMed=10501978;  
 RX Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dieckrich W.F.;  
 RT "The mouse Nalp gene cluster on Chromosome 13 encodes several distinct  
 RT functional transcripts.\*"  
 RL Mamm. Genome 10:1032-1035(1999).  
 DR EMBL: AF135493; AAD56765.1; -  
 DR HSSP: Q13490; 10BH.  
 DR MGD: MGI:1298220; Bircle.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR: 3.  
 DR SMART: SM00238; BIR: 3.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; UNKNOWN\_2.  
 DR PROSITE: PSS0143; BIR\_REPEAT\_2; 3.  
 SQ SEQUENCE 597 AA; 68322 MW; 4042E3DE51A7F9A0 CRC64;

Query Match 43.6%; Score 134; DB 11; Length 597;  
 Best Local Similarity 46.3%; Pred. No. 6.9e-09;  
 Matches 25; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 2 ELYRSTSTFPAGVPVSESLARAGFYTYGVNDKVCFCGGLMDNMKLGDSF 55  
 DB 119 RVKFTINMPTRIPIQPEQLADAGFYTYGVNDKVCFCGGLMCRHESGDDP 169

DB 232 EELRMDMKPMQESFVGEALVAGFYTGKDIYRCFCGGCLENWAEQDDP 285

## RESULT 15

ID 088642 PRELIMINARY; PRT: 224 AA.  
 AC 088642;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).  
 GN RIAP1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid-10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WISTAR; TISSUE-OVARY, CORPUS LUTEUM;  
 RA Bradley C.K., Lareu R.R., Dharmarajan A.M.;  
 RT "Cloning and characterization of an inhibitor of apoptosis protein  
 (IAP) in the rat corpus luteum";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF081503; AAC32497.1; -  
 DR HSP: 013490; IOBH.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR: 2.  
 DR SMART: SM00238; BIR: 2.  
 DR PROSITE: PS50143; BIR\_REPEAT\_2; 3.  
 DR NON\_TER 1  
 FT 224  
 FT NON\_TER 1  
 SQ SEQUENCE 224 AA: 25209 MW: 213A52534D5B56A CRC64;

Query Match 42.7% Score 131; DB 11; Length 224;  
 Best Local Similarity 51.0%; Pred. No. 5, 9e-09;  
 Matches 26; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
 QY 5 RMSTYETPPAGVPPYSERSLARAGYTYTGNDKVCFCGGLMDNWKLGDSF 55  
 DB 173 RMRFTLPWSSVLVPEQLASNGFTYVDHNDVRCFCGCGICRCWEPDDP 223

Search completed: January 7, 2002, 16:03:53  
 Job time: 1412 sec